

Ch 9200

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/654,449

499 DATE: 11/14/2001

TIME: 15:14:55

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Input Set: A:\4085-226-27.ST25.txt

Output Set: N:\CRF3\11142001\I654449.raw

AUG 04 2003

TECH CENTER 1600/2900

3 <110> APPLICANT: Palmer, Michelle A.J.
4 Gee, Melissa
5 Tillotson, Bonnie
6 Chang, Xiao-Jia
8 <120> TITLE OF INVENTION: Receptor Function Assay for G-Protein Coupled Receptors and
Orphan
9 Receptors by Reporter Enzyme Mutant Complementation
11 <130> FILE REFERENCE: 4085-226-27 09/054499
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/654,449 09/054499
14 <141> CURRENT FILING DATE: 2000-09-01
16 <150> PRIOR APPLICATION NUMBER: US 60/180,669
17 <151> PRIOR FILING DATE: 2000-02-07
19 <160> NUMBER OF SEQ ID NOS: 5
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 6700
25 <212> TYPE: DNA
26 <213> ORGANISM: Artificial Sequence
28 <220> FEATURE:
29 <223> OTHER INFORMATION: Nucleotide sequence for pICAST ALC ✓
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1457)...(4486)
34 <400> SEQUENCE: 1
35 ctgcagcctg aatatgggcc aaacaggata tctgtggtaa gcagttcctg cccggctca 60
36 gggccaagaa cagatgaac agctgaatat gggccaaaca gatatctgt ggttaagcagt 120
37 tcctgccccg gctcaggccc aagaacagat ggtccccaga tgcggtccag ccctcagcag 180
38 tttcttagaga accatcagat gttccaggg tgcccaagg acctgaaatg accctgtgcc 240
39 ttatgtAACAC taaccaatca gtcgcgttct cgcttctgtt cgcgcgcttc tgctccccga 300
40 gctcaataaa agagccaca acccctact cggggcaca gtcctccgat tgactgagtc 360
41 gcccgggtac ccgttatcc aataaaaccct cttgcagttt catccgactt gtggctcgc 420
42 tggccttgg gagggtctcc tctgagtgtat tgactacccg tcagcggggg tcttcattt 480
43 gggggctcgt cgggatcgg gagacccctg cccagggacc accgaccac caccggagg 540
44 caagctggcc agcaacttat ctgtgtctgt ccgattgtct agtgtctatg actgatttt 600
45 tgcgcctgcg tcggacttag ttagctaact agctctgtat ctggcggacc cgtgtggaa 660
46 ctgacgagtt ctgaacaccc ggcgcacaacc ctggagacg tcccaggac tttgggggcc 720
47 gttttgtgg cccgacctga ggaaggaggt cgatgtggaa tccgaccccg tcagatatg 780
48 tggccttggt aggagacgag aacctaaaac agttcccgcc tccgtctgaa ttttgcttt 840
49 cggtttggaa ccgaagccgc gctgtttgtc tgctgcagca tggtctgtt ttgtctgt 900
50 ctgactgtgt ttctgtatgt tgctgaaaat tagggccaga ctgttaccac tcccttaagt 960
51 ttgaccttag gtaactggaa agatgtcgag cggctcgctc acaaccagtc ggtagatgtc 1020
52 aagaagagac gttgggttae ettetgetct gcagaatggc caacctttaa cgtcgatgg 1080
53 cccgcgacg gcaccttaa ccgagaccc atcaccagg ttaagatcaa ggtctttca 1140
54 cctggccccc atggacaccc agaccaggtc ccctacatcg tgacctggaa agccttggct 1200
55 tttgacccccc ctccctgggt caagccctt gtacacccta agcctccggc tcctcttct 1260
56 ccatccgccc cgtctctccc ccttgaacct cctcggtcga ccccgctcg atcctccctt 1320
57 tatccagccc tcactccttc tetaggcgcc ggccgctcta gcccattaat acgactca 1380
58 atagggcgat tcgaatcagg ccttggcgcc cggatcctt attaagcgc aattggagg 1440
59 tggcggtac ctcgag atg ggc gtg att acg gat tca ctg gcc gtc gtg gcc 1492

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60	Met	Gly	Val	Ile	Thr	Asp	Ser	Leu	Ala	Val	Val	Ala					
61	1				5					10							
63	cgc	acc	gat	cgc	cct	tcc	caa	cag	tta	cgc	agc	ctg	aat	ggc	gaa	tgg	1540
64	Arg	Thr	Asp	Arg	Pro	Ser	Gln	Gln	Leu	Arg	Ser	Leu	Asn	Gly	Glu	Trp	
65	15				20					25							
67	cgc	ttt	gcc	tgg	ttt	ccg	gca	cca	gaa	gcg	gtg	ccg	gaa	agc	tgg	ctg	1588
68	Arg	Phe	Ala	Trp	Phe	Pro	Ala	Pro	Glu	Ala	Val	Pro	Glu	Ser	Trp	Leu	
69	30				35				40								
71	gag	tgc	gat	ctt	cct	gag	gcc	gat	act	gtc	gtc	ccc	tca	aac	tgg	1636	
72	Glu	Cys	Asp	Leu	Pro	Glu	Ala	Asp	Thr	Val	Val	Val	Pro	Ser	Asn	Trp	
73	45				50				55			60					
75	cag	atg	cac	ggt	tac	gat	gcg	ccc	atc	tac	acc	aac	gtg	acc	tat	ccc	1684
76	Gln	Met	His	Gly	Tyr	Asp	Ala	Pro	Ile	Tyr	Thr	Asn	Val	Thr	Tyr	Pro	
77		65				70				75							
79	att	acg	gtc	aat	ccg	ccg	ttt	gtt	ccc	acg	gag	aat	ccg	acg	ggt	tgt	1732
80	Ile	Thr	Val	Asn	Pro	Pro	Phe	Val	Pro	Thr	Glu	Asn	Pro	Thr	Gly	Cys	
81		80			85				90								
83	tac	tcg	ctc	aca	ttt	aat	gtt	gat	gaa	agc	tgg	cta	cag	gaa	ggc	cag	1780
84	Tyr	Ser	Leu	Thr	Phe	Asn	Val	Asp	Glu	Ser	Trp	Leu	Gln	Glu	Gly	Gln	
85		95			100				105								
87	acg	cga	att	att	ttt	gat	ggc	gtt	aac	tcg	gcg	ttt	cat	ctg	tgg	tgc	1828
88	Thr	Arg	Ile	Ile	Phe	Asp	Gly	Val	Asn	Ser	Ala	Phe	His	Leu	Trp	Cys	
89		110			115				120								
91	aac	ggg	cgc	tgg	gtc	ggt	tac	ggc	cag	gac	agt	cgt	ttg	ccg	tct	gaa	1876
92	Asn	Gly	Arg	Trp	Val	Gly	Tyr	Gly	Gln	Asp	Ser	Arg	Leu	Pro	Ser	Glu	
93	125				130				135			140					
95	ttt	gac	ctg	agc	gca	ttt	tta	cgc	gcc	gga	gaa	aac	cgc	ctc	gcg	gtg	1924
96	Phe	Asp	Leu	Ser	Ala	Phe	Leu	Arg	Ala	Gly	Glu	Asn	Arg	Leu	Ala	Val	
97		145			150				155								
99	atg	gtg	ctg	cgc	tgg	agt	gac	ggc	agt	tat	ctg	gaa	gat	cag	gat	atg	1972
100	Met	Val	Leu	Arg	Trp	Ser	Asp	Gly	Ser	Tyr	Leu	Glu	Asp	Gln	Asp	Met	
101		160			165				170								
103	tgg	cg	atg	agc	ggc	att	tcc	cgt	gac	gtc	tcg	ttg	ctg	cat	aaa	ccg	2020
104	Trp	Arg	Met	Ser	Gly	Ile	Phe	Arg	Asp	Val	Ser	Leu	Leu	His	Lys	Pro	
105		175			180				185								
107	act	aca	caa	atc	agc	gat	tcc	cat	gtt	gcc	act	cgc	ttt	aat	gat	gat	2068
108	Thr	Thr	Gln	Ile	Ser	Asp	Phe	His	Val	Ala	Thr	Arg	Phe	Asn	Asp	Asp	
109		190			195				200								
111	ttc	agc	cgc	gct	gta	ctg	gag	gct	gaa	gtt	cag	atg	tgc	ggc	gag	ttg	2116
112	Phe	Ser	Arg	Ala	Val	Leu	Glu	Ala	Glu	Val	Gln	Met	Cys	Gly	Glu	Leu	
113	205				210				215			220					
115	cgt	gac	tac	cta	cg	gta	aca	gtt	tct	tta	tgg	cag	ggt	gaa	acg	cag	2164
116	Arg	Asp	Tyr	Leu	Arg	Val	Thr	Val	Ser	Leu	Trp	Gln	Gly	Glu	Thr	Gln	
117		225			230				235								
119	gtc	gcc	agc	ggc	acc	g	cgc	cct	ttc	ggc	ggt	gaa	att	atc	gat	gag	2212
120	Val	Ala	Ser	Gly	Thr	Ala	Pro	Phe	Gly	Gly	Glu	Ile	Ile	Asp	Glu	Arg	
121		240			245				250								
123	ggt	ggt	tat	gcc	gat	cgc	gtc	aca	cta	cgt	ctg	aac	gtc	gaa	aac	ccg	2260
124	Gly	Gly	Tyr	Ala	Asp	Arg	Val	Thr	Leu	Arg	Leu	Asn	Val	Glu	Asn	Pro	

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127	aaa ctg tgg agc gcc gaa atc ccg aat ctc tat cgt gcg gtg gtt gaa			2308
128	Lys Leu Trp Ser Ala Glu Ile Pro Asn Leu Tyr Arg Ala Val Val Glu			
129	270	275	280	
131	ctg cac acc gcc gac ggc acg ctg att gaa gca gaa gcc tgc gat gtc			2356
132	Leu His Thr Ala Asp Gly Thr Leu Ile Glu Ala Glu Ala Cys Asp Val			
133	285	290	295	300
135	ggt ttc cgc gag gtg cgg att gaa aat ggt ctg ctg ctg aac ggc			2404
136	Gly Phe Arg Glu Val Arg Ile Glu Asn Gly Leu Leu Leu Leu Asn Gly			
137	305	310	315	
139	aag ccg ttg ctg att cga ggc gtt aac cgt cac gag cat cat cct ctg			2452
140	Lys Pro Leu Leu Ile Arg Gly Val Asn Arg His Glu His His Pro Leu			
141	320	325	330	
143	cat ggt cag gtc atg gat gag cag acg atg gtg cag gat atc ctg ctg			2500
144	His Gly Gln Val Met Asp Glu Gln Thr Met Val Gln Asp Ile Leu Leu			
145	335	340	345	
147	atg aag cag aac aac ttt aac gcc gtg cgc tgt tcg cat tat ccg aac			2548
148	Met Lys Gln Asn Asn Phe Asn Ala Val Arg Cys Ser His Tyr Pro Asn			
149	350	355	360	
151	cat ccg ctg tgg tac acg ctg tgc gac cgc tac ggc ctg tat gtg gtg			2596
152	His Pro Leu Trp Tyr Thr Leu Cys Asp Arg Tyr Gly Leu Tyr Val Val			
153	365	370	375	380
155	gat gaa gcc aat att gaa acc cac ggc atg gtg cca atg aat cgt ctg			2644
156	Asp Glu Ala Asn Ile Glu Thr His Gly Met Val Pro Met Asn Arg Leu			
157	385	390	395	
159	acc gat gat ccg cgc tgg cta ccg gcg atg agc gaa cgc gta acg cga			2692
160	Thr Asp Asp Pro Arg Trp Leu Pro Ala Met Ser Glu Arg Val Thr Arg			
161	400	405	410	
163	atg gtg cag cgc gat cgt aat cac ccg agt gtg atc atc tgg tcg ctg			2740
164	Met Val Gln Arg Asp Arg Asn His Pro Ser Val Ile Ile Trp Ser Leu			
165	415	420	425	
167	ggg aat gaa tca ggc cac ggc gct aat cac gac gcg ctg tat cgc tgg			2788
168	Gly Asn Glu Ser Gly His Gly Ala Asn His Asp Ala Leu Tyr Arg Trp			
169	430	435	440	
171	atc aaa tct gtc gat cct tcc cgc ccg gtg cag tat gaa ggc ggc gga			2836
172	Ile Lys Ser Val Asp Pro Ser Arg Pro Val Gln Tyr Glu Gly Gly			
173	445	450	455	460
175	gcc gac acc acg gcc acc gat att att tgc ccg atg tac gcg cgc gtg			2884
176	Ala Asp Thr Thr Ala Thr Asp Ile Ile Cys Pro Met Tyr Ala Arg Val			
177	465	470	475	
179	gat gaa gac cag ccc ttc ccg gct gtg cgc aaa tgg tcc atc aaa aaa			2932
180	Asp Glu Asp Gln Pro Phe Pro Ala Val Pro Lys Trp Ser Ile Lys Lys			
181	480	485	490	
183	tgg ctt tcg cta cct gga gag acg cgc ccg ctg atc ctt tgc gaa tac			2980
184	Trp Leu Ser Leu Pro Gly Glu Thr Arg Pro Leu Ile Leu Cys Glu Tyr			
185	495	500	505	
187	gcc cac gcg atg ggt aac agt ctt ggc ggt ttc gct aaa tac tgg cag			3028
188	Ala His Ala Met Gly Asn Ser Leu Gly Gly Phe Ala Lys Tyr Trp Gln			
189	510	515	520	

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191	gcg	ttt	cgt	cag	tat	ccc	cgt	tta	cag	ggc	ggc	ttc	gtc	tgg	gac	tgg	3076
192	Ala	Phe	Arg	Gln	Tyr	Pro	Arg	Leu	Gln	Gly	Gly	Phe	Val	Trp	Asp	Trp	
193	525					530				535					540		
195	gtg	gat	cag	tcg	ctg	att	aaa	tat	gat	gaa	aac	ggc	aac	ccg	tgg	tcg	3124
196	Val	Asp	Gln	Ser	Leu	Ile	Lys	Tyr	Asp	Glu	Asn	Gly	Asn	Pro	Trp	Ser	
197						545				550					555		
199	gct	tac	ggc	ggt	gat	ttt	ggc	gat	acg	ccg	aac	gat	ccg	cag	ttc	tgt	3172
200	Ala	Tyr	Gly	Gly	Asp	Phe	Gly	Asp	Thr	Pro	Asn	Asp	Arg	Gln	Phe	Cys	
201						560				565					570		
203	atg	aac	ggt	ctg	gtc	ttt	gcc	gac	ccg	acg	ccg	cat	cca	gcg	ctg	acg	3220
204	Met	Asn	Gly	Leu	Val	Phe	Ala	Asp	Arg	Thr	Pro	His	Pro	Ala	Leu	Thr	
205						575				580					585		
207	gaa	gca	aaa	cac	cag	cag	cag	ttt	ttc	cag	ttc	cgt	tta	tcc	ggg	caa	3268
208	Glu	Ala	Lys	His	Gln	Gln	Gln	Phe	Phe	Gln	Phe	Arg	Leu	Ser	Gly	Gln	
209						590				595					600		
211	acc	atc	gaa	gtg	acc	agc	gaa	tac	ctg	ttc	cgt	cat	agc	gat	aac	gag	3316
212	Thr	Ile	Glu	Val	Thr	Ser	Glu	Tyr	Leu	Phe	Arg	His	Ser	Asp	Asn	Glu	
213						605				610					620		
215	ctc	ctg	cac	tgg	atg	gtg	gcg	ctg	gat	ggt	aag	ccg	ctg	gca	agc	ggt	3364
216	Leu	Leu	His	Trp	Met	Val	Ala	Leu	Asp	Gly	Lys	Pro	Leu	Ala	Ser	Gly	
217						625				630					635		
219	gaa	gtg	cct	ctg	gat	gtc	gct	cca	caa	ggt	aaa	cag	ttg	att	gaa	ctg	3412
220	Glu	Val	Pro	Leu	Asp	Val	Ala	Pro	Gln	Gly	Lys	Gln	Leu	Ile	Glu	Leu	
221						640				645					650		
223	cct	gaa	cta	ccg	cag	ccg	gag	agc	gcc	ggg	caa	ctc	tgg	ctc	aca	gtt	3460
224	Pro	Glu	Leu	Pro	Gln	Pro	Glu	Ser	Ala	Gly	Gln	Leu	Trp	Leu	Thr	Val	
225						655				660					665		
227	cgc	gta	gtg	caa	ccg	aac	gcg	acc	gca	tgg	tca	gaa	gcc	ggg	cac	atc	3508
228	Arg	Val	Val	Gln	Pro	Asn	Ala	Thr	Ala	Trp	Ser	Glu	Ala	Gly	His	Ile	
229						670				675					680		
231	agc	gcc	tgg	cag	cag	ttg	cgt	ctg	gcg	gaa	aac	ctc	agt	gtg	acg	ctc	3556
232	Ser	Ala	Trp	Gln	Gln	Trp	Arg	Leu	Ala	Glu	Asn	Leu	Ser	Val	Thr	Leu	
233						685				690					700		
235	ccc	gcc	gcg	tcc	cac	gcc	atc	ccg	cat	ctg	acc	acc	agc	gaa	atg	gat	3604
236	Pro	Ala	Ala	Ser	His	Ala	Ile	Pro	His	Leu	Thr	Thr	Ser	Glu	Met	Asp	
237						705				710					715		
239	ttt	tgc	atc	gag	ctg	ggt	aat	aag	cgt	ttg	caa	ttt	aac	ccg	cag	tca	3652
240	Phe	Cys	Ile	Glu	Leu	Gly	Asn	Lys	Arg	Trp	Gln	Phe	Asn	Arg	Gln	Ser	
241						720				725					730		
243	ggc	ttt	ctt	tca	cag	atg	tgg	att	ggc	gat	aaa	aaa	caa	ctg	ctg	acg	3700
244	Gly	Phe	Leu	Ser	Gln	Met	Trp	Ile	Gly	Asp	Lys	Lys	Gln	Leu	Leu	Thr	
245						735				740					745		
247	ccg	ctg	cgc	gat	cag	ttc	acc	cgt	gca	ccg	ctg	gat	aac	gac	att	ggc	3748
248	Pro	Leu	Arg	Asp	Gln	Phe	Thr	Arg	Ala	Pro	Leu	Asp	Asn	Asp	Ile	Gly	
249						750				755					760		
251	gta	agt	gaa	qcg	acc	cgc	att	gac	ect	aat	ccg	tgg	gtc	gaa	cgc	tgg	3796
252	Val	Ser	Glu	Ala	Thr	Arg	Ile	Asp	Pro	Asn	Ala	Trp	Val	Glu	Arg	Trp	
253						765				770					780		
255	aag	gcg	gca	cat	tac	cag	gcc	gaa	gca	gcg	ttg	ttg	cag	tgc	acg		3844

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256	Lys	Ala	Ala	Gly	His	Tyr	Gln	Ala	Glu	Ala	Ala	Leu	Leu	Gln	Cys	Thr	
257							785					790				795	
259	gca	gat	aca	ctt	gct	gat	gcg	gtg	ctg	att	acg	acc	gct	cac	gcg	tgg	3892
260	Ala	Asp	Thr	Leu	Ala	Asp	Ala	Val	Leu	Ile	Thr	Thr	Ala	His	Ala	Trp	
261							800				805				810		
263	cag	cat	cag	ggg	aaa	acc	tta	ttt	atc	agc	cg	aaa	acc	tac	cg	att	3940
264	Gln	His	Gln	Gly	Lys	Thr	Leu	Phe	Ile	Ser	Arg	Lys	Thr	Tyr	Arg	Ile	
265							815			820			825				
267	gat	gg	agt	gg	caa	atg	gcg	att	acc	gtt	gat	gtt	gaa	gtg	gcg	agc	3988
268	Asp	Gly	Ser	Gly	Gln	Met	Ala	Ile	Thr	Val	Asp	Val	Glu	Val	Ala	Ser	
269							830			835			840				
271	gat	aca	ccg	cat	ccg	gcg	cg	att	ggc	ctg	aac	tgc	cag	ctg	gcg	cag	4036
272	Asp	Thr	Pro	His	Pro	Ala	Arg	Ile	Gly	Leu	Asn	Cys	Gln	Leu	Ala	Gln	
273	845						850				855			860			
275	gta	gca	gag	cg	gt	aa	tcg	ctc	gga	tta	gg	ccg	caa	gaa	aac	tat	4084
276	Val	Ala	Glu	Arg	Val	Asn	Trp	Leu	Gly	Leu	Gly	Pro	Gln	Glu	Asn	Tyr	
277							865			870			875				
279	ccc	gac	cgc	ctt	act	gcc	gc	tgt	ttt	gac	cg	tgg	gat	ctg	cca	ttg	4132
280	Pro	Asp	Arg	Leu	Thr	Ala	Ala	Cys	Phe	Asp	Arg	Trp	Asp	Leu	Pro	Leu	
281							880			885			890				
283	tca	gac	atg	tat	acc	ccg	tac	gtc	ttc	ccg	agc	gaa	aac	gg	ctg	cg	4180
284	Ser	Asp	Met	Tyr	Thr	Pro	Tyr	Val	Phe	Pro	Ser	Glu	Asn	Gly	Leu	Arg	
285							895			900			905				
287	tgc	gg	acg	cg	gaa	ttg	aat	ttt	ggc	cca	cac	cag	tgg	cg	gg	gac	4228
288	Cys	Gly	Thr	Arg	Glu	Leu	Asn	Tyr	Gly	Pro	His	Gln	Trp	Arg	Gly	Asp	
289							910			915			920				
291	tcc	cag	tcc	aa	atc	agc	cg	tac	agt	caa	cag	caa	ctg	atg	gaa	acc	4276
292	Phe	Gln	Phe	Asn	Ile	Ser	Arg	Tyr	Ser	Gln	Gln	Gln	Leu	Met	Glu	Thr	
293	925						930				935			940			
295	agc	cat	cgc	cat	ctg	ctg	cac	gcg	gaa	gaa	ggc	aca	tgg	ctg	aat	atc	4324
296	Ser	His	Arg	His	Leu	Leu	His	Ala	Glu	Glu	Gly	Thr	Trp	Leu	Asn	Ile	
297							945			950			955				
299	gac	gg	tcc	cat	atg	gg	att	gg	ggc	gac	gac	tcc	tgg	agc	ccg	tca	4372
300	Asp	Gly	Phe	His	Met	Gly	Ile	Gly	Gly	Asp	Asp	Ser	Trp	Ser	Pro	Ser	
301							960			965			970				
303	gta	tcg	gcg	gaa	tcc	cag	ctg	agc	gc	gg	tac	cat	tac	cag	ttg		4420
304	Val	Ser	Ala	Glu	Phe	Gln	Leu	Ser	Ala	Gly	Arg	Tyr	His	Tyr	Gln	Leu	
305							975			980			985				
307	gtc	tgg	tgt	caa	aaa	aga	tct	gac	tat	aaa	gat	gag	gac	ctc	gac	cat	4468
308	Val	Trp	Cys	Gln	Lys	Arg	Ser	Asp	Tyr	Lys	Asp	Glu	Asp	Leu	Asp	His	
309							990			995			1000				
311	cat	cat	cat	cac	cg	taataatagg											4516
312	His	His	His	His	His	Arg											
313	1005					1010											
315	tgcattgtatc	cctcgaccaa	tcccggttat	tttccaccat	at	tgccgtct	tttggcaat										4576
316	tgagggeee	gaaacctggc	cctgtcttct	tgacgagcat	tccttaggggt	cttccccc	c										4636
317	tgc	ccaaagg	aatgcaaggt	ctgttgaatg	tcgtgaagga	agcagttcct	ctggaa	gct									4696
318	ctt	gaagaca	aacaacgtct	gtatcgaccc	tttgcaggca	gcggaa	cccc	ccac	ctggc								4756
319	acagg	tcgtgc	ccaa	aagccacgtg	tataagatac	ac	tgca	aa	g								4816

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/654,449

DATE: 11/14/2001
TIME: 15:14:56

Input Set : A:\4085-226-27.ST25.txt
Output Set: N:\CRF3\11142001\I654449.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number